

AMENDMENTS TO THE CLAIMS

1.– 13. (Cancelled)

14. (Currently Amended) A computer-implemented method of generating a local-global alignment score which indicates a global and a local similarity between a first protein structure and a second protein structure, the method executed by one or more computer systems and comprising:

receiving, at the one or more computer systems, a protein structure correspondence wherein a plurality of positions in the protein structure correspondence indicates a corresponding pair of residues in the first protein structure and the second protein structure;

the one or more computer systems determining a plurality of root mean square deviations corresponding to a plurality of sets of pairs of residues, wherein each set of pairs of residues comprises a plurality of pairs of residues that are contiguous in the protein structure correspondences and the plurality of root mean square deviations are determined using a plurality of specified threshold values;

the one or more computer systems selecting a longest contiguous segment corresponding to a set of pairs of residues of the plurality of pairs of residues based on the plurality of root mean square deviations

the one or more computer systems identifying a plurality of distance

scores, wherein each distance score corresponds to a number
of pairs of residues in the correspondence that are within a
pre-defined distance of a plurality of pre-defined distances

the one or more computer systems selecting a global distance test

value based on the plurality of distance scores;

the one or more computer systems generating the local-global

alignment score based on the longest contiguous segment and
the global distance test value ; and

the one or more computer systems providing a result based on the

local-global alignment score.

15. (Cancelled)

16. (Cancelled)

17. (Cancelled)

18. (Cancelled)

19. (Currently Amended) The method of claim 14, wherein the one or more

computer systems comprise a server and further comprising:

receiving, at a server, a first set of co-ordinates associated with the first
protein structure from a client;

receiving, at the server, a second set of co-ordinates associated the second
protein structure; and

the server generating, ~~at the server~~, the protein structure correspondence

based on the first set of co-ordinates and the second set of co-ordinates.

20. (Currently Amended) The method of claim 14, further comprising:

receiving, at the one or more computer systems, a first set of co-ordinates associated with the first protein structure;

receiving, at the one or more computer systems, a second set of co-ordinates associated the second protein structure; and

the one or more computer systems generating the protein structure correspondence based on the first set of co-ordinates and the second set of co-ordinates.

21. (Currently Amended) The method of claim 20, wherein providing a result based on the local-global alignment score further comprises:

the one or more computer systems generating a second protein structure correspondence based on the local-global alignment score; and

the one or more computer systems providing the second protein structure correspondence.

22. (Currently Amended) The method of claim 20, wherein providing the second protein structure correspondence comprises:

the one or more computer systems modifying the set of co-ordinates

specifying the first protein structure based on at least one of the global

distance test value and the longest continuous segment to generate a

second set of co-ordinates specifying the first protein structure; and

the one or more computer systems providing the second modified set of co-ordinates.

23. (Currently Amended) The method of claim 21, wherein providing the second protein structure correspondence comprises:

the one or more computer systems displaying a graphical representation of at

least one of the first protein structure or the second protein structure,

wherein at least some of the residues in the graphical representation

are colored according to distance between the at least some of the

residues and the corresponding residues in the second protein

structure.

24. (Previously Presented) The method of claim 23, wherein the graphical representation is a bar plot.

25. (Previously Presented) The method of claim 23, wherein the graphical representation is a three-dimensional protein structure.